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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/668,314A

Input Set : A:\6280NCPseq.txt

Output Set: C:\CRF3\05242001\I668314A.raw

4 <110> APPLICANT: Gurney, Mark
 5 Bienkowski, Michael J.
 7 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
 USES

8 THEREOF
 10 <130> FILE REFERENCE: 28341/6280NCP
 12 <140> CURRENT APPLICATION NUMBER: 09/668,314A
 13 <141> CURRENT FILING DATE: 2000-09-22
 15 <150> PRIOR APPLICATION NUMBER: 60/169,232
 16 <151> PRIOR FILING DATE: 1999-12-06
 18 <150> PRIOR APPLICATION NUMBER: 09/416,901
 19 <151> PRIOR FILING DATE: 1999-10-13
 21 <150> PRIOR APPLICATION NUMBER: 60/155,493
 22 <151> PRIOR FILING DATE: 1999-09-23
 24 <150> PRIOR APPLICATION NUMBER: 09/404,133
 25 <151> PRIOR FILING DATE: 1999-09-23
 27 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881
 28 <151> PRIOR FILING DATE: 1999-09-23
 30 <150> PRIOR APPLICATION NUMBER: 60/101,594
 31 <151> PRIOR FILING DATE: 1998-09-24
 33 <160> NUMBER OF SEQ ID NOS: 82
 35 <170> SOFTWARE: PatentIn Ver. 2.0
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 39 <212> TYPE: DNA
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 66 cagtcttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
 67 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccggtgtca gcgtcgcccc 1500
 68 cgtgaccctg aggtcgtaa tgatgagtcc tctctggtca gacatcgctg gaaatgaata 1560
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 71 gctcccagat gccttctaga ttcactgtct tttgattctt gattttcaag ctttcaaatac 1740
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 85 20 25 30
 87 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
 88 35 40 45
 90 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
 91 50 55 60
 93 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
 94 65 70 75 80
 96 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
 97 85 90 95
 99 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
 100 100 105 110
 102 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
 103 115 120 125
 105 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
 106 130 135 140
 108 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
 109 145 150 155 160
 111 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
 112 165 170 175
 115 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
 116 180 185 190
 118 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
 119 195 200 205
 121 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
 122 210 215 220
 124 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
 125 225 230 235 240
 128 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
 129 245 250 255
 131 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
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 137 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
 138 290 295 300
 140 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
 141 305 310 315 320
 143 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
 144 325 330 335
 146 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
 147 340 345 350
 149 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
 150 355 360 365
 152 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
 153 370 375 380
 155 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
 156 385 390 395 400
 158 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
 159 405 410 415
 161 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
 162 420 425 430
 164 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
 165 435 440 445
 167 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
 168 450 455 460
 171 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
 172 465 470 475 480
 174 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
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 192 ctgcggctgc cccgggagac cgacgaagag cccgaggagc cccggccggag gggcagcttt 180
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 200 ctggtaaagc agacccacgt tcccaaccc ttctccctgc acctttgtgg tgctggcttc 660
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 204 tacaactatg acaagagcat tgtggacagt ggcaccacca acttcgaaa gcccaagaaa 900
 205 gtgttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
 206 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttgaaacatt 1020
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 208 atccttccgc agcaataacct gcggccagtg gaagatgtgg ccacgtcccc agacgactgt 1140
 209 tacaagtttgc ccatctcaca gtcattccacg ggcactgtta tggagactgt tatcatggag 1200
 210 ggcttctacg ttgtcttga tcgggcccga aaacgaattt gctttgtgt cagcgcttgc 1260
 211 catgtgcacg atgagttcag gacggcagcg gtggaaaggcc cttttgtcac cttggacatg 1320
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 219 ctttggtcacc tcaaattttaa gtcggaaat tctgctgctt gaaacttcag ccctgaacct 1800
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 221 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaaccct ggcagagaag 1920
 222 agaccaagct tgttccctg ctggccaaag tcagtaggag agatgcaca gtttgctatt 1980
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 238 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 239 35 40 45
 241 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 242 50 55 60
 244 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 245 65 70 75 80
 247 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 248 85 90 95
 250 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 251 100 105 110
 254 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 255 115 120 125
 257 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 258 130 135 140
 260 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 261 145 150 155 160
 263 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp

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270	195	200	205
272	Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln		
273	210	215	220
275	Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile		
276	225	230	240
278	Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg		
279	245	250	255
282	Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln		
283	260	265	270
285	Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val		
286	275	280	285
288	Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala		
289	290	295	300
291	Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp		
292	305	310	315
294	Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr		
295	325	330	335
297	Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val		
298	340	345	350
300	Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg		
301	355	360	365
303	Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala		
304	370	375	380
306	Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu		
307	385	390	395
309	Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala		
310	405	410	415
312	Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu		
313	420	425	430
315	Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro		
316	435	440	445
318	Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala		
319	450	455	460
321	Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp		
322	465	470	475
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VERIFICATION SUMMARY

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